

SEQUENCE LISTING

<110> MORIKAWA, NORIYUKI
NISHIKAWA, TETSUO
OTA, TOSHIO
ISOGAI, TAKAO
HIO, YURI
MASUHO, YASUHIKO

<120> FATTY ACID TRANSPORTER PROTEINS AND THE GENES ENCODING
THE PROTEINS

<130> 084335-0154

<140> 10/030,226
<141> 2002-01-08

<150> PCT/JP00/04549
<151> 2000-07-07

<150> JP 2000/128993
<151> 2000-04-25

<150> JP 11/194179
<151> 1999-07-08

<150> 60/159,586
<151> 1999-10-18

<160> 15

<170> PatentIn Ver. 2.1

<210> 1
<211> 2405
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (59)..(2248)

<400> 1
gcactcctcc cgggtttctg ctctccgccc gtgtggagtg gtggggcct gggtggga 58
atg ggc gtg tgc cag cgc acg cgc gct ccc tgg aag gag aag tct cag 106
Met Gly Val Cys Gln Arg Thr Arg Ala Pro Trp Lys Glu Lys Ser Gln
1 5 10 15
cta gaa cga gcg gcc cta ggt ttt cgg aag gga gga tca ggg atg ttt 154
Leu Glu Arg Ala Ala Leu Gly Phe Arg Lys Gly Ser Gly Met Phe
20 25 30
gcg agc ggc tgg aac cag acg gtg ccg ata gag gaa gcg ggc tcc atg 202
Ala Ser Gly Trp Asn Gln Thr Val Pro Ile Glu Glu Ala Gly Ser Met
35 40 45

gct gcc ctc ctg ctg ccc ctg ctg ttg cta ccg ctg ctg ctg Ala Ala Leu Leu Leu Leu Pro Leu Leu Leu Leu Leu Pro Leu Leu 50 55 60	250
ctg aag cta cac ctc tgg ccg cag ttg cgc tgg ctt ccg gcg gac ttg Leu Lys Leu His Leu Trp Pro Gln Leu Arg Trp Leu Pro Ala Asp Leu 65 70 75 80	298
gcc ttt gcg gtg cga gct ctg tgc tgc aaa agg gct ctt cga gct cgc Ala Phe Ala Val Arg Ala Leu Cys Cys Lys Arg Ala Leu Arg Ala Arg 85 90 95	346
gcc ctg gcc gcg gct gcc gac ccg gaa ggt ccc gag ggg ggc tgc Ala Leu Ala Ala Ala Ala Asp Pro Glu Gly Pro Glu Gly Gly Cys 100 105 110	394
agc ctg gcc tgg cgc ctc gcg gaa ctg gcc cag cag cgc gcc gcg cac Ser Leu Ala Trp Arg Leu Ala Glu Leu Ala Gln Gln Arg Ala Ala His 115 120 125	442
acc ttt ctc att cac ggc tcg cgg cgc ttt agc tac tca gag gcg gag Thr Phe Leu Ile His Gly Ser Arg Arg Phe Ser Tyr Ser Glu Ala Glu 130 135 140	490
cgc gag agt aac agg gct gca cgc gcc ttc cta cgt gcg cta ggc tgg Arg Glu Ser Asn Arg Ala Ala Arg Ala Phe Leu Arg Ala Leu Gly Trp 145 150 155 160	538
gac tgg gga ccc gac ggc gac agc ggc gag ggg agc gct gga gaa Asp Trp Gly Pro Asp Gly Gly Asp Ser Gly Glu Gly Ser Ala Gly Glu 165 170 175	586
ggc gag cgg gca gcg ccg gga gcc gga gat gca gcg gcc gga agc ggc Gly Glu Arg Ala Ala Pro Gly Ala Gly Asp Ala Ala Gly Ser Gly 180 185 190	634
gcg gag ttt gcc gga ggg gac ggt gcc gcc aga ggt gga gga gcc gcc Ala Glu Phe Ala Gly Gly Asp Gly Ala Ala Arg Gly Gly Ala Ala 195 200 205	682
gcc cct ctg tca cct gga gca act gtg gcg ctg ctc ctc ccc gct ggc Ala Pro Leu Ser Pro Gly Ala Thr Val Ala Leu Leu Leu Pro Ala Gly 210 215 220	730
cca gag ttt ctg tgg ctc tgg ttc ggg ctg gcc aag gcc ggc ctg cgc Pro Glu Phe Leu Trp Leu Trp Phe Gly Leu Ala Lys Ala Gly Leu Arg 225 230 235 240	778
act gcc ttt gtg ccc acc gcc ctg cgc cgg ggc ccc ctg ctg cac tgc Thr Ala Phe Val Pro Thr Ala Leu Arg Arg Gly Pro Leu Leu His Cys 245 250 255	826
ctc cgc agc tgc ggc gcg cgc gcg ctg gtg ctg gcg cca gag ttt ctg Leu Arg Ser Cys Gly Ala Arg Ala Leu Val Leu Ala Pro Glu Phe Leu 260 265 270	874

gag tcc ctg gag ccg gac ctg ccc gcc ctg aga gcc atg ggg ctc cac Glu Ser Leu Glu Pro Asp Leu Pro Ala Leu Arg Ala Met Gly Leu His 275 280 285	922
ctg tgg gct gca ggc cca gga acc cac cct gct gga att agc gat ttg Leu Trp Ala Ala Gly Pro Gly Thr His Pro Ala Gly Ile Ser Asp Leu 290 295 300	970
ctg gct gaa gtg tcc gct gaa gtg gat ggg cca gtg cca gga tac ctc Leu Ala Glu Val Ser Ala Glu Val Asp Gly Pro Val Pro Gly Tyr Leu 305 310 315 320	1018
tct tcc ccc cag agc ata aca gac acg tgc ctg tac atc ttc acc tct Ser Ser Pro Gln Ser Ile Thr Asp Thr Cys Leu Tyr Ile Phe Thr Ser 325 330 335	1066
ggc acc acg ggc ctc ccc aag gct gct cggt atc agt cat ctg aag atc Gly Thr Thr Gly Leu Pro Lys Ala Ala Arg Ile Ser His Leu Lys Ile 340 345 350	1114
ctg caa tgc cag ggc ttc tat cag ctg tgt ggt gtc cac cag gaa gat Leu Gln Cys Gln Gly Phe Tyr Gln Leu Cys Gly Val His Gln Glu Asp 355 360 365	1162
gtg atc tac ctc gcc ctc cca ctc tac cac atg tcc ggt tcc ctg ctg Val Ile Tyr Leu Ala Leu Pro Leu Tyr His Met Ser Gly Ser Leu Leu 370 375 380	1210
ggc atc gtg ggc tgc atg ggc att ggg gcc aca gtg gtg ctg aaa tcc Gly Ile Val Gly Cys Met Gly Ile Gly Ala Thr Val Val Leu Lys Ser 385 390 395 400	1258
aag ttc tcg gct ggt cag ttc tgg gaa gat tgc cag cag cac agg gtg Lys Phe Ser Ala Gly Gln Phe Trp Glu Asp Cys Gln Gln His Arg Val 405 410 415	1306
acg gtg ttc cag tac att ggg gag ctg tgc cga tac ctt gtc aac cag Thr Val Phe Gln Tyr Ile Gly Glu Leu Cys Arg Tyr Leu Val Asn Gln 420 425 430	1354
ccc ccg agc aag gca gaa cgt ggc cat aag gtc cgg ctg gca gtg ggc Pro Pro Ser Lys Ala Glu Arg Gly His Lys Val Arg Leu Ala Val Gly 435 440 445	1402
agc ggg ctg cgc cca gat acc tgg gag cgt ttt gtg cgg cgc ttc ggg Ser Gly Leu Arg Pro Asp Thr Trp Glu Arg Phe Val Arg Arg Phe Gly 450 455 460	1450
ccc ctg cag gtg ctg gag aca tat gga ctg aca gag ggc aac gtg gcc Pro Leu Gln Val Leu Glu Thr Tyr Gly Leu Thr Glu Gly Asn Val Ala 465 470 475 480	1498
acc atc aac tac aca gga cag cgg ggc gct gtg ggg cgt gct tcc tgg Thr Ile Asn Tyr Thr Gly Gln Arg Gly Ala Val Gly Arg Ala Ser Trp 485 490 495	1546

ctt tac aag cat atc ttc ccc ttc tcc ttg att cgc tat gat gtc acc Leu Tyr Lys His Ile Phe Pro Phe Ser Leu Ile Arg Tyr Asp Val Thr 500 505 510	1594
aca gga gag cca att cg ^g gac ccc cag ggg cac tgt atg gcc aca tct Thr Gly Glu Pro Ile Arg Asp Pro Gln Gly His Cys Met Ala Thr Ser 515 520 525	1642
cca ggt gag cca ggg ctg ctg gtg gcc ccg gta agc cag cag tcc cca Pro Gly Glu Pro Gly Leu Leu Val Ala Pro Val Ser Gln Gln Ser Pro 530 535 540	1690
t ^t c ctg ggc tat gct ggc ggg cca gag ctg gcc cag ggg aag ttg cta Phe Leu Gly Tyr Ala Gly Pro Glu Leu Ala Gln Gly Lys Leu Leu 545 550 555 560	1738
aag gat gtc ttc cgg cct ggg gat gtt ttc ttc aac act ggg gac ctg Lys Asp Val Phe Arg Pro Gly Asp Val Phe Phe Asn Thr Gly Asp Leu 565 570 575	1786
ctg gtc tgc gat gac caa ggt ttt ctc cgc ttc cat gat cgt act gga Leu Val Cys Asp Asp Gln Gly Phe Leu Arg Phe His Asp Arg Thr Gly 580 585 590	1834
gac acc ttc agg tgg aag ggg gag aat gtg gcc aca acc gag gtg gca Asp Thr Phe Arg Trp Lys Gly Glu Asn Val Ala Thr Thr Glu Val Ala 595 600 605	1882
gag gtc ttc gag gcc cta gat ttt ctt cag gag gtg aac gtc tat gga Glu Val Phe Glu Ala Leu Asp Phe Leu Gln Glu Val Asn Val Tyr Gly 610 615 620	1930
g ^t c act gtg cca ggg cat gaa ggc agg gct gga atg gca gcc cta gtt Val Thr Val Pro Gly His Glu Gly Arg Ala Gly Met Ala Ala Leu Val 625 630 635 640	1978
ctg cgt ccc ccc cac gct ttg gac ctt atg cag ctc tac acc cac gtg Leu Arg Pro Pro His Ala Leu Asp Leu Met Gln Leu Tyr Thr His Val 645 650 655	2026
tct gag aac ttg cca cct tat gcc cgg ccc cga ttc ctc agg ctc cag Ser Glu Asn Leu Pro Pro Tyr Ala Arg Pro Arg Phe Leu Arg Leu Gln 660 665 670	2074
gag tct ttg gcc acc aca gag acc ttc aaa cag cag aaa gtt cgg atg Glu Ser Leu Ala Thr Thr Glu Thr Phe Lys Gln Gln Lys Val Arg Met 675 680 685	2122
gca aat gag ggc ttc gac ccc agc acc ctg tct gac cca ctg tac gtt Ala Asn Glu Gly Phe Asp Pro Ser Thr Leu Ser Asp Pro Leu Tyr Val 690 695 700	2170
ctg gac cag gct gta ggt gcc tac ctg ccc ctc aca act gcc cgg tac Leu Asp Gln Ala Val Gly Ala Tyr Leu Pro Leu Thr Thr Ala Arg Tyr 705 710 715 720	2218

agc gcc ctc ctg gca gga aac ctt cga atc tgagaacttc cacacctgag 2268
 Ser Ala Leu Leu Ala Gly Asn Leu Arg Ile
 725 730

gcacctgaga gaggaactct gtggggtggg ggccgttgca ggtgtactgg gctgtcaggg 2328
 atctttctta taccagaact gcggtcacta ttttctaata aatgtggctg gagctgatcc 2388
 agctgtctct gacctac 2405

<210> 2
 <211> 730
 <212> PRT
 <213> Homo sapiens

<400> 2
 Met Gly Val Cys Gln Arg Thr Arg Ala Pro Trp Lys Glu Lys Ser Gln
 1 5 10 15

Leu Glu Arg Ala Ala Leu Gly Phe Arg Lys Gly Ser Gly Met Phe
 20 25 30

Ala Ser Gly Trp Asn Gln Thr Val Pro Ile Glu Glu Ala Gly Ser Met
 35 40 45

Ala Ala Leu Leu Leu Leu Pro Leu Leu Leu Leu Pro Leu Leu Leu
 50 55 60

Leu Lys Leu His Leu Trp Pro Gln Leu Arg Trp Leu Pro Ala Asp Leu
 65 70 75 80

Ala Phe Ala Val Arg Ala Leu Cys Cys Lys Arg Ala Leu Arg Ala Arg
 85 90 95

Ala Leu Ala Ala Ala Ala Asp Pro Glu Gly Pro Glu Gly Gly Cys
 100 105 110

Ser Leu Ala Trp Arg Leu Ala Glu Leu Ala Gln Gln Arg Ala Ala His
 115 120 125

Thr Phe Leu Ile His Gly Ser Arg Arg Phe Ser Tyr Ser Glu Ala Glu
 130 135 140

Arg Glu Ser Asn Arg Ala Ala Arg Ala Phe Leu Arg Ala Leu Gly Trp
 145 150 155 160

Asp Trp Gly Pro Asp Gly Gly Asp Ser Gly Glu Gly Ser Ala Gly Glu
 165 170 175

Gly Glu Arg Ala Ala Pro Gly Ala Gly Asp Ala Ala Ala Gly Ser Gly
 180 185 190

Ala Glu Phe Ala Gly Gly Asp Gly Ala Ala Arg Gly Gly Ala Ala
 195 200 205

Ala Pro Leu Ser Pro Gly Ala Thr Val Ala Leu Leu Leu Pro Ala Gly
 210 215 220

Pro Glu Phe Leu Trp Leu Trp Phe Gly Leu Ala Lys Ala Gly Leu Arg
 225 230 235 240
 Thr Ala Phe Val Pro Thr Ala Leu Arg Arg Gly Pro Leu Leu His Cys
 245 250 255
 Leu Arg Ser Cys Gly Ala Arg Ala Leu Val Leu Ala Pro Glu Phe Leu
 260 265 270
 Glu Ser Leu Glu Pro Asp Leu Pro Ala Leu Arg Ala Met Gly Leu His
 275 280 285
 Leu Trp Ala Ala Gly Pro Gly Thr His Pro Ala Gly Ile Ser Asp Leu
 290 295 300
 Leu Ala Glu Val Ser Ala Glu Val Asp Gly Pro Val Pro Gly Tyr Leu
 305 310 315 320
 Ser Ser Pro Gln Ser Ile Thr Asp Thr Cys Leu Tyr Ile Phe Thr Ser
 325 330 335
 Gly Thr Thr Gly Leu Pro Lys Ala Ala Arg Ile Ser His Leu Lys Ile
 340 345 350
 Leu Gln Cys Gln Gly Phe Tyr Gln Leu Cys Gly Val His Gln Glu Asp
 355 360 365
 Val Ile Tyr Leu Ala Leu Pro Leu Tyr His Met Ser Gly Ser Leu Leu
 370 375 380
 Gly Ile Val Gly Cys Met Gly Ile Gly Ala Thr Val Val Leu Lys Ser
 385 390 395 400
 Lys Phe Ser Ala Gly Gln Phe Trp Glu Asp Cys Gln Gln His Arg Val
 405 410 415
 Thr Val Phe Gln Tyr Ile Gly Glu Leu Cys Arg Tyr Leu Val Asn Gln
 420 425 430
 Pro Pro Ser Lys Ala Glu Arg Gly His Lys Val Arg Leu Ala Val Gly
 435 440 445
 Ser Gly Leu Arg Pro Asp Thr Trp Glu Arg Phe Val Arg Arg Phe Gly
 450 455 460
 Pro Leu Gln Val Leu Glu Thr Tyr Gly Leu Thr Glu Gly Asn Val Ala
 465 470 475 480
 Thr Ile Asn Tyr Thr Gly Gln Arg Gly Ala Val Gly Arg Ala Ser Trp
 485 490 495
 Leu Tyr Lys His Ile Phe Pro Phe Ser Leu Ile Arg Tyr Asp Val Thr
 500 505 510
 Thr Gly Glu Pro Ile Arg Asp Pro Gln Gly His Cys Met Ala Thr Ser
 515 520 525

Pro Gly Glu Pro Gly Leu Leu Val Ala Pro Val Ser Gln Gln Ser Pro
 530 535 540
 Phe Leu Gly Tyr Ala Gly Gly Pro Glu Leu Ala Gln Gly Lys Leu Leu
 545 550 555 560
 Lys Asp Val Phe Arg Pro Gly Asp Val Phe Phe Asn Thr Gly Asp Leu
 565 570 575
 Leu Val Cys Asp Asp Gln Gly Phe Leu Arg Phe His Asp Arg Thr Gly
 580 585 590
 Asp Thr Phe Arg Trp Lys Gly Glu Asn Val Ala Thr Thr Glu Val Ala
 595 600 605
 Glu Val Phe Glu Ala Leu Asp Phe Leu Gln Glu Val Asn Val Tyr Gly
 610 615 620
 Val Thr Val Pro Gly His Glu Gly Arg Ala Gly Met Ala Ala Leu Val
 625 630 635 640
 Leu Arg Pro Pro His Ala Leu Asp Leu Met Gln Leu Tyr Thr His Val
 645 650 655
 Ser Glu Asn Leu Pro Pro Tyr Ala Arg Pro Arg Phe Leu Arg Leu Gln
 660 665 670
 Glu Ser Leu Ala Thr Thr Glu Thr Phe Lys Gln Gln Lys Val Arg Met
 675 680 685
 Ala Asn Glu Gly Phe Asp Pro Ser Thr Leu Ser Asp Pro Leu Tyr Val
 690 695 700
 Leu Asp Gln Ala Val Gly Ala Tyr Leu Pro Leu Thr Thr Ala Arg Tyr
 705 710 715 720
 Ser Ala Leu Leu Ala Gly Asn Leu Arg Ile
 725 730

```

<210> 3
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Combined DNA/RNA Molecule: Artificially
      synthesized oligo-cap linker

<220>
<223> Description of Artificial Sequence: Artificially
      synthesized oligo-cap linker

<400> 3
agcaucgagu cggccuuguu ggccuacugg

```

```
<210> 4
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificially
      synthesized primer sequence

<400> 4
gcggctgaag acggcctatg tggcctttt tttttttt tt          42

<210> 5
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificially
      synthesized primer sequence

<400> 5
agcatcgagt cggcattgtt g          21

<210> 6
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificially
      synthesized primer sequence

<400> 6
gcggctgaag acggcctatg t          21

<210> 7
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificially
      synthesized primer sequence

<400> 7
ggaattccgt ggagtggatgg gggcctgggt gggaat          36

<210> 8
<211> 39
<212> DNA
<213> Artificial Sequence
```

<220>
 <223> Description of Artificial Sequence: Artificially
 synthesized primer sequence

<400> 8
 cgggatccca cctgcaacgg cccccacccc acagagttc

39

<210> 9
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Artificially
 synthesized primer sequence

<400> 9
 ggaattccgt ggagtggtgg gggcctgggt gggaat

36

<210> 10
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Artificially
 synthesized primer sequence

<400> 10
 cgggatccga ttcaagggtt tcctgccag

29

<210> 11
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Artificially
 synthesized primer sequence

<400> 11
 aacagggtcg cacgcgcctt

20

<210> 12
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Artificially
 synthesized primer sequence

<400> 12
 cgggatccca cctgcaacgg cccccacccc acagagttc

39

<210> 13
<211> 1748
<212> DNA
<213> Mus sp.

<400> 13
acggcgccga ggcgttttagc tacgcggagg ctgagcgcga gagcaaccgg attgctcgcg 60
ccttctcgcg cgacacggggc tggaccgggg gcccggcagg ctcgggcagg ggcagcactg 120
aggaaggcgc acgcgtggcg cctccggctg gagatgcggc tgctagaggg acgaccgcgc 180
ccccctctggc acccgggggcg accgtggcgc tgctctccc agcgggcccgg gatttcctt 240
ggatgggtt cgactggcc aaagctggcc tgccgcacggc ctttgtgccc accgctttac 300
gccgaggacc cctgctgcac tgccctccga gctgcgggtgc gagtgccgtc gtgctggcca 360
cagagtccctg ggagtcctg gagccggacc tgccggcctt gagagccatg gggctccacc 420
tatgggcgac gggccctgaa actaatgttag ctggaatcag caatttgcta tcggaagcaq 480
cagaccaagt ggtatgagcca gtgcgggggt accctctctgc ccccccagaac ataatggaca 540
cctgcctgtatcatcttcacc tctggacta ctggcctgccc caaggctgtc cgaatcagtc 600
atctgaaggt tctacagtgc cagggattct accatctgtg tggagttccac caggaggacg 660
tgcgttacact cgcactccca ctgttaccaca tgcgttggcgc cttctggcattgtggct 720
gtttggcat tggggccacc gtgggtgtga aacccaagtt ctcagctgc cagttctggg 780
acgattgcca gaaacacagg gtgacagtgt tccagttacat tggggagttg tgccgatacc 840
tcgtcaacca gccccccgagc aaggcagagt ttgaccataa ggtgcgttgc gcaagtggca 900
gtgggttgcg cccagacacc tggggagcggtt tccgtggcgc atttggacact ctgcagatac 960
tggagacgta tggcatgaca gagggaacg tagctacgtt caatttacaca ggacggcagg 1020
gtgcagtggg ggcggatccatc tggcttaca agcacatctt ccccttctcc ttgattcgat 1080
acgatgtcat gacagggggag cctattcga atgcccaggg gcactgcgt accacatctc 1140
cagggtgagcc aggccactgtg tggggccccc tgagccagca gtccccccttc ctgggtatg 1200
ctggggctcc ggagctggcc aaggacaagg tgcgttgcgg tgcgttgcgg tctggggacg 1260
ttttcttcaa tactggggac ctcttgcgtt gtgttgcgtt aggcttctt cacttccacg 1320
atcgtaactgg agacaccatc aggttggaaagg gagagaatgt ggccacaact gaagtggctg 1380
aggcttttgcg gaccctggac ttcccttcagg aggttgcgtt ctatggagtc acgggtgccag 1440
ggcacgaagg cagggcaggg atggcgccct tgcgttgcgg gccccccgcgg gctctgaacc 1500
tggtgcatcttccatc ttttgcgtt gtttgcgtt acttgcacc gtatggccgg cctcggtttc 1560
tcaggctcca ggaatctttg gccactactg agaccccttcaa acagcagaag gttaggatgg 1620
ccaatgaggg ctttgaccccttgg agtgtactgt ctgacccact ctatgttgc gaccaagata 1680
taggggccta cctgcccccttccatc acacctggccgg ggtacagtgc cctccgttgc ggagaccccttccatc 1740
gaatctga 1748

<210> 14
<211> 614
<212> PRT
<213> Mus sp.

<400> 14
Ala Ala Ala Asp Pro Glu Ser Ser Glu Ser Gly Cys Ser Leu Ala Trp
1 5 10 15
Arg Leu Ala Tyr Leu Ala Arg Glu Gln Pro Thr His Thr Phe Leu Ile
20 25 30
His Gly Ala Gln Arg Phe Ser Tyr Ala Glu Ala Glu Arg Glu Ser Asn
35 40 45
Arg Ile Ala Arg Ala Phe Leu Arg Ala Arg Gly Trp Thr Gly Gly Arg
50 55 60

Arg Gly Ser Gly Arg Gly Ser Thr Glu Glu Gly Ala Arg Val Ala Pro
 65 70 75 80

Pro Ala Gly Asp Ala Ala Ala Arg Gly Thr Thr Ala Pro Pro Leu Ala
 85 90 95

Pro Gly Ala Thr Val Ala Leu Leu Pro Ala Gly Pro Asp Phe Leu
 100 105 110

Trp Ile Trp Phe Gly Leu Ala Lys Ala Gly Leu Arg Thr Ala Phe Val
 115 120, 125

Pro Thr Ala Leu Arg Arg Gly Pro Leu Leu His Cys Leu Arg Ser Cys
 130 135 140

Gly Ala Ser Ala Leu Val Leu Ala Thr Glu Phe Leu Glu Ser Leu Glu
 145 150 155 160

Pro Asp Leu Pro Ala Leu Arg Ala Met Gly Leu His Leu Trp Ala Thr
 165 170 175

Gly Pro Glu Thr Asn Val Ala Gly Ile Ser Asn Leu Leu Ser Glu Ala
 180 185 190

Ala Asp Gln Val Asp Glu Pro Val Pro Gly Tyr Leu Ser Ala Pro Gln
 195 200 205

Asn Ile Met Asp Thr Cys Leu Tyr Ile Phe Thr Ser Gly Thr Thr Gly
 210 215 220

Leu Pro Lys Ala Ala Arg Ile Ser His Leu Lys Val Leu Gln Cys Gln
 225 230 235 240

Gly Phe Tyr His Leu Cys Gly Val His Gln Glu Asp Val Ile Tyr Leu
 245 250 255

Ala Leu Pro Leu Tyr His Met Ser Gly Ser Leu Leu Gly Ile Val Gly
 260 265 270

Cys Leu Gly Ile Gly Ala Thr Val Val Leu Lys Pro Lys Phe Ser Ala
 275 280 285

Ser Gln Phe Trp Asp Asp Cys Gln Lys His Arg Val Thr Val Phe Gln
 290 295 300 320

Tyr Ile Gly Glu Leu Cys Arg Tyr Leu Val Asn Gln Pro Pro Ser Lys
 305 310 315

Ala Glu Phe Asp His Lys Val Arg Leu Ala Val Gly Ser Gly Leu Arg
 325 330 335

Pro Asp Thr Trp Glu Arg Phe Leu Arg Arg Phe Gly Pro Leu Gln Ile
 340 345 350

Leu Glu Thr Tyr Gly Met Thr Glu Gly Asn Val Ala Thr Phe Asn Tyr
 355 360 365

Thr Gly Arg Gln Gly Ala Val Gly Arg Ala Ser Trp Leu Tyr Lys His
 370 375 380

 Ile Phe Pro Phe Ser Leu Ile Arg Tyr Asp Val Met Thr Gly Glu Pro
 385 390 395 400

 Ile Arg Asn Ala Gln Gly His Cys Met Thr Thr Ser Pro Gly Glu Pro
 405 410 415

 Gly Leu Leu Val Ala Pro Val Ser Gln Gln Ser Pro Phe Leu Gly Tyr
 420 425 430

 Ala Gly Ala Pro Glu Leu Ala Lys Asp Lys Leu Leu Lys Asp Val Phe
 435 440 445

 Trp Ser Gly Asp Val Phe Phe Asn Thr Gly Asp Leu Leu Val Cys Asp
 450 455 460

 Glu Gln Gly Phe Leu His Phe His Asp Arg Thr Gly Asp Thr Ile Arg
 465 470 475 480

 Trp Lys Gly Glu Asn Val Ala Thr Thr Glu Val Ala Glu Val Leu Glu
 485 490 495

 Thr Leu Asp Phe Leu Gln Glu Val Asn Ile Tyr Gly Val Thr Val Pro
 500 505 510

 Gly His Glu Gly Arg Ala Gly Met Ala Ala Leu Ala Leu Arg Pro Pro
 515 520 525

 Gln Ala Leu Asn Leu Val Gln Leu Tyr Ser His Val Ser Glu Asn Leu
 530 535 540

 Pro Pro Tyr Ala Arg Pro Arg Phe Leu Arg Leu Gln Glu Ser Leu Ala
 545 550 555 560

 Thr Thr Glu Thr Phe Lys Gln Gln Lys Val Arg Met Ala Asn Glu Gly
 565 570 575

 Phe Asp Pro Ser Val Leu Ser Asp Pro Leu Tyr Val Leu Asp Gln Asp
 580 585 590

 Ile Gly Ala Tyr Leu Pro Leu Thr Pro Ala Arg Tyr Ser Ala Leu Leu
 595 600 605

 Ser Gly Asp Leu Arg Ile
 610

<210> 15
 <211> 620
 <212> PRT
 <213> Homo sapiens

<400> 15
 Met Leu Ser Ala Ile Tyr Thr Val Leu Ala Gly Leu Leu Phe Leu Pro
 1 5 10 15

Leu	Leu	Val	Asn	Leu	Cys	Cys	Pro	Tyr	Phe	Phe	Gln	Asp	Ile	Gly	Tyr
				20					25				30		
Phe	Leu	Lys	Val	Ala	Ala	Val	Gly	Arg	Arg	Val	Arg	Ser	Tyr	Gly	Gln
		35				40				45					
Arg	Arg	Pro	Ala	Arg	Thr	Ile	Leu	Arg	Ala	Phe	Leu	Glu	Lys	Ala	Arg
		50				55					60				
Gln	Thr	Pro	His	Lys	Pro	Phe	Leu	Leu	Phe	Arg	Asp	Glu	Thr	Leu	Thr
		65			70				75				80		
Tyr	Ala	Gln	Val	Asp	Arg	Arg	Ser	Asn	Gln	Val	Ala	Arg	Ala	Leu	His
		85						90					95		
Asp	His	Leu	Gly	Leu	Arg	Gln	Gly	Asp	Cys	Val	Ala	Leu	Leu	Met	Gly
		100						105					110		
Asn	Glu	Pro	Ala	Tyr	Val	Trp	Leu	Trp	Leu	Gly	Leu	Val	Lys	Leu	Gly
		115					120					125			
Cys	Ala	Met	Ala	Cys	Leu	Asn	Tyr	Asn	Ile	Arg	Ala	Lys	Ser	Leu	Leu
		130				135					140				
His	Cys	Phe	Gln	Cys	Cys	Gly	Ala	Lys	Val	Leu	Leu	Val	Ser	Pro	Glu
		145			150				155				160		
Leu	Gln	Ala	Ala	Val	Glu	Glu	Ile	Leu	Pro	Ser	Leu	Lys	Lys	Asp	Asp
		165						170				175			
Val	Ser	Ile	Tyr	Tyr	Val	Ser	Arg	Thr	Ser	Asn	Thr	Asp	Gly	Ile	Asp
		180						185				190			
Ser	Phe	Leu	Asp	Lys	Val	Asp	Glu	Val	Ser	Thr	Glu	Pro	Ile	Pro	Glu
		195					200					205			
Ser	Trp	Arg	Ser	Glu	Val	Thr	Phe	Ser	Thr	Pro	Ala	Leu	Tyr	Ile	Tyr
		210				215					220				
Thr	Ser	Gly	Thr	Thr	Gly	Leu	Pro	Lys	Ala	Ala	Met	Ile	Thr	His	Gln
		225			230				235				240		
Arg	Ile	Trp	Tyr	Gly	Thr	Gly	Leu	Thr	Phe	Val	Ser	Gly	Leu	Lys	Ala
		245						250					255		
Asp	Asp	Val	Ile	Tyr	Ile	Thr	Leu	Pro	Phe	Tyr	His	Ser	Ala	Ala	Leu
		260					265					270			
Leu	Ile	Gly	Ile	His	Gly	Cys	Ile	Val	Ala	Gly	Ala	Thr	Leu	Ala	Leu
		275					280					285			
Arg	Thr	Lys	Phe	Ser	Ala	Ser	Gln	Phe	Trp	Asp	Asp	Cys	Arg	Lys	Tyr
		290					295					300			
Asn	Val	Thr	Val	Ile	Gln	Tyr	Ile	Gly	Glu	Leu	Leu	Arg	Tyr	Leu	Cys
		305			310				315				320		

Asn Ser Pro Gln Lys Pro Asn Asp Arg Asp His Lys Val Arg Leu Ala
 325 330 335
 Leu Gly Asn Gly Leu Arg Gly Asp Val Trp Arg Gln Phe Val Lys Arg
 340 345 350
 Phe Gly Asp Ile Cys Ile Tyr Glu Phe Tyr Ala Ala Thr Glu Gly Asn
 355 360 365
 Ile Gly Phe Met Asn Tyr Ala Arg Lys Val Gly Ala Val Gly Arg Val
 370 375 380
 Asn Tyr Leu Gln Lys Lys Ile Ile Thr Tyr Asp Leu Ile Lys Tyr Asp
 385 390 395 400
 Val Glu Lys Asp Glu Pro Val Arg Asp Glu Asn Gly Tyr Cys Val Arg
 405 410 415
 Val Pro Lys Gly Glu Val Gly Leu Leu Val Cys Lys Ile Thr Gln Leu
 420 425 430
 Thr Pro Phe Asn Gly Tyr Ala Gly Ala Lys Ala Gln Thr Glu Lys Lys
 435 440 445
 Lys Leu Arg Asp Val Phe Lys Lys Gly Asp Leu Tyr Phe Asn Ser Gly
 450 455 460
 Asp Leu Leu Met Val Asp His Glu Asn Phe Ile Tyr Phe His Asp Arg
 465 470 475 480
 Val Gly Asp Thr Phe Arg Trp Lys Gly Glu Asn Val Ala Thr Thr Glu
 485 490 495
 Val Ala Asp Thr Val Gly Leu Val Asp Phe Val Gln Glu Val Asn Val
 500 505 510
 Tyr Gly Val His Val Pro Asp His Glu Gly Arg Ile Gly Met Ala Ser
 515 520 525
 Ile Lys Met Lys Glu Asn His Glu Phe Asp Gly Lys Lys Leu Phe Gln
 530 535 540
 His Ile Ala Asp Tyr Leu Pro Ser Tyr Ala Arg Pro Arg Phe Leu Arg
 545 550 555 560
 Ile Gln Asp Thr Ile Glu Ile Thr Gly Thr Phe Lys His Arg Lys Met
 565 570 575
 Thr Leu Val Glu Glu Gly Phe Asn Pro Ala Val Ile Lys Asp Ala Leu
 580 585 590
 Tyr Phe Leu Asp Asp Thr Ala Lys Met Tyr Val Pro Met Thr Glu Asp
 595 600 605
 Ile Tyr Asn Ala Ile Ser Ala Lys Thr Leu Lys Leu
 610 615 620